

2.13.2K	GACATCCAGA	TGACCCAGTT	TCCATCCTCC	CTGTC	TGCAT	CTGTAGGAGA	50
A30	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTC	TGCAT	CTGTAGGAGA	50
2.14.3K	-----	-----	----TCCTCC	CTGTC	TGCAT	CTGTAGGAGA	26
2.12.1K	-----	-----	-----	-----	TGCAT	CTGTAGGAGA	15
4.9.2K	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTC	TGCAT	CTGTAGGAGA	50
Consensus	GACATCCAGA	TGACCCAGTY	TCCATCCTCC	CTGTC	TGCAT	CTGTAGGAGA	50
CDR1							
2.13.2K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGGCATTAGA	AA	TGATTTAG	100
A30	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGGCATTAGA	AA	TGATTTAG	100
2.14.3K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGGCATTAGA	CG	TGATTTAG	76
2.12.1K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGGCATTAGA	CG	TGATTTAG	65
4.9.2K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGGCATTAGA	AG	TGATTTAG	100
Consensus	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGGCATTAGA	MR	TGATTTAG	100
2.13.2K	GCTGGTTTCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	150	150
A30	GCTGGTTTCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	150	150
2.14.3K	GCTGGTTTCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	126	126
2.12.1K	GCTGGTTTCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	115	115
4.9.2K	GCTGGTTTCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	150	150
Consensus	GCTGGTTTCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	150	150
CDR2							
2.13.2K	GCATCCAGTT	TTCACAGTGG	GGTCCCATCA	AGGTTACGCG	GCAGTGGATC	200	200
A30	GCATCCAGTT	TTCACAGTGG	GGTCCCATCA	AGGTTACGCG	GCAGTGGATC	200	200
2.14.3K	GCATCCAGTT	TTCACAGTGG	GGTCCCATCA	AGGTTACGCG	GCAGTGGATC	176	176
2.12.1K	GCATCCAGTT	TTCACAGTGG	GGTCCCATCA	AGGTTACGCG	GCAGTGGATC	165	165
4.9.2K	GCATCCAAAT	TTCACAGTGG	GGTCCCATCA	AGGTTACGCG	GCAGTGGATC	200	200
Consensus	GCATCCARWT	TTCACAGTGG	GGTCCCATCA	AGGTTACGCG	GCAGTGGATC	200	200
2.13.2K	TGGGACAGAA	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT	GAAGATTTTG	250	250
A30	TGGGACAGAA	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT	GAAGATTTTG	250	250
2.14.3K	TGGGACAGAA	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT	GAAGATTTTG	226	226
2.12.1K	TGGGACAGAA	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT	GAAGATTTTG	215	215
4.9.2K	TGGGACAGAA	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT	GAAGATTTTG	250	250
Consensus	TGGGACAGAA	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT	GAAGATTTTG	250	250
CDR3							
2.13.2K	CAACTTATTA	CTGTCTACAG	CATAATAGTT	ACCGTGCGAG	TTTTGGGCCAG	300	300
A30	CAACTTATTA	CTGTCTACAG	CATAATAGTT	ACCG-TCCN-	-----	288	288
2.14.3K	CAACTTATTA	CTGTCTACAG	CATAATAGTT	ATCCTCGGAC	GTTCGGGCCAA	276	276
2.12.1K	CAACTTATTA	CTGTCTACAG	CATAATAGTT	ATCCTCGGAC	GTTCGGGCCAA	265	265
4.9.2K	CAACTTATTA	CTGTCTACAG	CATAATAGTT	ACCGTCTCAC	TTTCGGGCGGA	300	300
Consensus	CAACTTATTA	CTGTCTACAG	CATAATAGTT	ATCCKYESNS	KTTYGGGCSRR	300	300
2.13.2K	GGGACCAAGC	TGGAGATCAA	AC----			322	322
A30	-----	-----	-----			288	288
2.14.3K	GGGACCGAGG	TGGAAATCAT	ACGAAC			302	302
2.12.1K	GGGACCGAGG	TGGAAATCAT	ACGAAC			291	291
4.9.2K	GGGACCAAGG	TGGAGATCAA	AC----			322	322
Consensus	GGGACCRAGE	TGGARATCAW	ACGAAC			326	326

FIG. 1A

4.17.3K	-----	-----	-----	-----	AGGAGA	7
O12	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	50
Consensus	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	50
	CDR1					
4.17.3K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GAGCATTAGT	ACCTTTTAA	57
O12	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GAGCATTAGC	AGCTATTTAA	100
Consensus	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GAGCATTAGY	ASCTATTTAA	100
4.17.3K	ATTGGTATCA	GCAGAAACCA	GGGAAAGCCC	CTAACTCCT	GATCATGTT	107
O12	ATTGGTATCA	GCAGAAACCA	GGGAAAGCCC	CTAACTCCT	GATCATGCT	150
Consensus	ATTGGTATCA	GCAGAAACCA	GGGAAAGCCC	CTAACTCCT	GATCATGCT	150
	CDR2					
4.17.3K	GCATCCAGTT	TCAAGGTGG	GGTCCCATCA	AGGTTCAGTG	GCAGTGGATC	157
O12	GCATCCAGTT	TCAAGGTGG	GGTCCCATCA	AGGTTCAGTG	GCAGTGGATC	200
Consensus	GCATCCAGTT	TCAAGGTGG	GGTCCCATCA	AGGTTCAGTG	GCAGTGGATC	200
4.17.3K	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG	207
O12	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG	250
Consensus	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG	250
	CDR3					
4.17.3K	CAACTTACTA	CTGTCAACAG	AGTTACAGT	CCCCACTCAC	TTTCGGCGGA	257
O12	CAACTTACTA	CTGTCAACAG	AGTTACAGT	CCCC-TCC-	-----	288
Consensus	CAACTTACTA	CTGTCAACAG	AGTTACAGT	CCCCAYYCH	TTTCGGCGGA	300
4.17.3K	GGGACCAAGG	TGGAGATCAA	AC			279
O12	-----	-----	--			288
Consensus	GGGACCAAGG	TGGAGATCAA	AC			322

FIG. 1B

6.1.1K	-----	-----	-----	-----	-----	50
A27	GAAATTGTGT	TGACGCAGTC	TCCAGGCACC	CTGTCTTTGT	CTCCAGGGGA	50
Consensus	GAAATTGTGT	TGACGCAGTC	TCCAGGCACC	CTGTCTTTGT	CTCCAGGGGA	
			CDR1			
6.1.1K	-AGAGCCACC	CTCTCCTGTA	GGGCCAGTCA	GAGTGTTGC	GGCAGGTA	49
A27	AGAGCCACC	CTCTCCTGTA	GGGCCAGTCA	GAGTGTTAGC	AGCAGGTA	100
Consensus	AGAGCCACC	CTCTCCTGTA	GGGCCAGTCA	GAGTGTTGC	AGCAGGTA	100
6.1.1K						
A27	TAGCCTGGTA	CCAGCAGAAA	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	99
Consensus	TAGCCTGGTA	CCAGCAGAAA	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	150
			CDR2			150
6.1.1K	GGTGCATCCA	GCAGGGCCAC	TGGCATCCCA	GACAGGTTCA	GTGGCAGTGG	149
A27	GGTGCATCCA	GCAGGGCCAC	TGGCATCCCA	GACAGGTTCA	GTGGCAGTGG	200
Consensus	GGTGCATCCA	GCAGGGCCAC	TGGCATCCCA	GACAGGTTCA	GTGGCAGTGG	200
6.1.1K	GTCTGGGACA	GACTTCACTC	TCACCATCAG	CAGACTGGAG	CCTGAAGATT	199
A27	GTCTGGGACA	GACTTCACTC	TCACCATCAG	CAGACTGGAG	CCTGAAGATT	250
Consensus	GTCTGGGACA	GACTTCACTC	TCACCATCAG	CAGACTGGAG	CCTGAAGATT	250
			CDR3			
6.1.1K	TTGCAGTGT	TTACTGTCAG	CAGTATGGTA	GTTCACCTCG	NACGTTCCGGC	249
A27	TTGCAGTGT	TTACTGTCAG	CAGTATGGTA	GTTCACCTCC	-----	290
Consensus	TTGCAGTGT	TTACTGTCAG	CAGTATGGTA	GTTCACCTCS	NACGTTCCGGC	300
6.1.1K	CAAGGGACCA	AGGTGGAAAT	CAAAC			274
A27	-----	-----	-----			290
Consensus	CAAGGGACCA	AGGTGGAAAT	CAAAC			325

FIG. 1C

2.12.1H	-----	GGGAGGC	TTGGTCAAGC	CTGGA	GGTC	26	
DP35	CAGGTGCAGC	TGGTGGAGTC	TGGGGGAGGC	TTGGTCAAGC	CTGGA	GGTC	50
Consensus	CAGGTGCAGC	TGGTGGAGTC	TGGGGGAGGC	TTGGTCAAGC	CTGGA	GGTC	50
CDR1							
2.12.1H	CCTGAGACTC	TCCTGTGCAG	CCTCTGGATT	CAC	TTTCAGT	GACTACTATA	76
DP35	CCTGAGACTC	TCCTGTGCAG	CCTCTGGATT	CAC	TTTCAGT	GACTACTACA	100
Consensus	CCTGAGACTC	TCCTGTGCAG	CCTCTGGATT	CAC	TTTCAGT	GACTACTATA	100
2.12.1H	TGAGCTGGAT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGATG	GGTTTCATAC	126	
DP35	TGAGCTGGAT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGATG	GGTTTCATAC	150	
Consensus	TGAGCTGGAT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGATG	GGTTTCATAC	150	
CDR2							
2.12.1H	ATTAGTAGTA	GTGGTAGTAC	CAGAG	ACTAC	GCAGACTCTG	TGAAGGGCCG	176
DP35	ATTAGTAGTA	GTGGTAGTAC	CAGAG	ACTAC	GCAGACTCTG	TGAAGGGCCG	200
Consensus	ATTAGTAGTA	GTGGTAGTAC	CAGAG	ACTAC	GCAGACTCTG	TGAAGGGCCG	200
2.12.1H	ATTACCATC	TCCAGGGACA	ACGCCAAGAA	CTCACTGTAT	CTGCAAATGA	226	
DP35	ATTACCATC	TCCAGGGACA	ACGCCAAGAA	CTCACTGTAT	CTGCAAATGA	250	
Consensus	ATTACCATC	TCCAGGGACA	ACGCCAAGAA	CTCACTGTAT	CTGCAAATGA	250	
2.12.1H	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTGT	ATTACTGTGT	GAGAGATGGA	276	
DP35	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTGT	ATTACTGTGT	GAGAGATGGA	296	
Consensus	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTGT	ATTACTGTGT	GAGAGATGGA	300	
CDR3							
2.12.1H	GTGGAAACTA	CTTTTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA	326	
DP35	GTGGAAACTA	CTTTTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA	296	
Consensus	GTGGAAACTA	CTTTTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA	350	
2.12.1H	AGGGACCACG	GTCACCGTCT	CCTCAG			352	
DP35	AGGGACCACG	GTCACCGTCT	CCTCAG			296	
Consensus	AGGGACCACG	GTCACCGTCT	CCTCAG			376	

FIG. 2A

PF2-2.14.3H.DNA	-----	GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC	30
VIV-4/4.35	CAGGTGCAGC TGCAGGAGTC	GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC	50
Consensus	CAGGTGCAGC TGCAGGAGTC	GGGCCCAGGA CTGGTGAAGC CTTCGGAGAC	50
		CDR1	
PF2-2.14.3H.DNA	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT	ATTACTACT	80
VIV-4/4.35	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT	ATTACTACT	100
Consensus	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT	ATTACTACT	100
	CDR1		
PF2-2.14.3H.DNA	GGAGCTGGAT CCGGCAGCCC GCCGGGAAGG GACTGGAGTG GATTGGGCGT		130
VIV-4/4.35	GGAGCTGGAT CCGGCAGCCC GCCGGGAAGG GACTGGAGTG GATTGGGCGT		150
Consensus	GGAGCTGGAT CCGGCAGCCC GCCGGGAAGG GACTGGAGTG GATTGGGCGT		150
	CDR2		
PF2-2.14.3H.DNA	ATCTATACCA GTGGGAGGCC CAACTACAAC CCTTCCCTCA AGAGTCGAGT		180
VIV-4/4.35	ATCTATACCA GTGGGAGGCC CAACTACAAC CCTTCCCTCA AGAGTCGAGT		200
Consensus	ATCTATACCA GTGGGAGGCC CAACTACAAC CCTTCCCTCA AGAGTCGAGT		200
PF2-2.14.3H.DNA	CACCATGTCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGACT		230
VIV-4/4.35	CACCATGTCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGACT		250
Consensus	CACCATGTCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGACT		250
PF2-2.14.3H.DNA	CTGTGACCGC CGCGGACACG GCCGTGTATT ACTGTGCGGT AACGATTTT		280
VIV-4/4.35	CTGTGACCGC CGCGGACACG GCCGTGTATT ACTGTGCGGT AACGATTTT		288
Consensus	CTGTGACCGC CGCGGACACG GCCGTGTATT ACTGTGCGGT AACGATTTT		300
	CDR3		
PF2-2.14.3H.DNA	GGAGTGGTTA TTATCTTTGA CTACTGGGGC CAGGGACCC TGGTCACCGT		330
VIV-4/4.35	-----	AGGAGT---	294
Consensus	GGAGTGGTTA TTATCTTTGA CTACTGGGGC CAGGGACCC TGGTCACCGT		350
PF2-2.14.3H.DNA	CTCCTCAG		338
VIV-4/4.35	-----		294
Consensus	CTCCTCAG		358

FIG. 2B

6.1.1H	GAGGTGCAGC	TGTTGGAGTC	TGCGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
4.9.2H	GAGGTGCAGC	TGTTGGAGTC	TGCGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
DP47	GAGGTGCAGC	TGTTGGAGTC	TGCGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
2.13.2H	GAGGTGCAGC	TGTTGGAGTC	TGCGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
Consensus	GAGGTGCAGC	TGTTGGAGTC	TGCGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
CDR1						
6.1.1H	CCTGAGACTC	TCCTGTSCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
4.9.2H	CCTGAGACTC	TCCTGTSCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
DP47	CCTGAGACTC	TCCTGTSCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
2.13.2H	CCTGAGACTC	TCCTGTSCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
Consensus	CCTGAGACTC	TCCTGTSCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
CDR1			CDR2			
6.1.1H	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGGT	150
4.9.2H	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGGT	150
DP47	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGGT	150
2.13.2H	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGGT	150
Consensus	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGGT	150
CDR2						
6.1.1H	ATTACTGGTA	GTGGTGGTAG	TACATCTAC	GCAGACTCCG	TGAAGGGCCG	200
4.9.2H	ATTACTGGTA	GTGGTGGTAG	TACATCTAC	GCAGACTCCG	TGAAGGGCCG	200
DP47	ATTACTGGTA	GTGGTGGTAG	TACATCTAC	GCAGACTCCG	TGAAGGGCCG	200
2.13.2H	ATTACTGGTA	GTGGTGGTAG	TACATCTAC	GCAGACTCCG	TGAAGGGCCG	200
Consensus	ATTACTGGTA	GTGGTGGTAG	TACATCTAC	GCAGACTCCG	TGAAGGGCCG	200
6.1.1H	GTTCAACATC	TCCAGAGACA	ATTCCAGCAA	CACGCTGTAT	CTGCAAAATGA	250
4.9.2H	GTTCAACATC	TCCAGAGACA	ATTCCAGCAA	CACGCTGTAT	CTGCAAAATGA	250
DP47	GTTCAACATC	TCCAGAGACA	ATTCCAGCAA	CACGCTGTAT	CTGCAAAATGA	250
2.13.2H	GTTCAACATC	TCCAGAGACA	ATTCCAGCAA	CACGCTGTAT	CTGCAAAATGA	250
Consensus	GTTCAACATC	TCCAGAGACA	ATTCCAGCAA	CACGCTGTAT	CTGCAAAATGA	250
CDR3						
6.1.1H	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAAGATCTC--	298
4.9.2H	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAAGATCTG	300
DP47	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAAGATCTG	296
2.13.2H	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAAGATCTT	300
Consensus	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAAGATCTK	300
CDR3-for 4.9.2 and 2.13.2						
6.1.1H	-----	-----	-----	-----	-----C-	299
4.9.2H	GGCTACGGTG	ACTTTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGGCCA	350
DP47	-----	-----	-----	-----	-----	296
2.13.2H	GGCTGGTCCG	ACTCTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGGCCA	350
Consensus	GGCTRSKSYG	ACTYTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGGCCA	350
CDR3-for 6.1.1						
6.1.1H	AGGGACTACG	GTGATTATGA	GTTGGTTCGA	CCCCTGGGGC	CAGGGAACCC	349
4.9.2H	AGGGACCAC-	-----	-----	-----	-----	359
DP47	-----	-----	-----	-----	-----	296
2.13.2H	AGGGACCAC-	-----	-----	-----	-----	359
Consensus	AGGGACYACG	GTGATTATGA	GTTGGTTCGA	CCCCTGGGGC	CAGGGAACCC	400

FIG. 2C-1

6.1.1H	TGGTCACCGT CTCCTCAG	367
4.9.2H	-GGTCACCGT CTCCTCAG	376
DP47	-----	296
2.13.2H	-GGTCACCGT CTCCTCAG	376
Consensus	TGGTCACCGT CTCCTCAG	418

FIG. 2C-2

4.17.3H	-----	CCCAGGA CTGGTGAAGC CTTCCGAGAC	27
DP71	CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCCGAGAC		50
Consensus	CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCCGAGAC		50
		CDR1	
4.17.3H	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT		77
DP71	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT		100
Consensus	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT		100
		CDR1	
4.17.3H	GGAGTTGGAT CCGGCAGCCC CCAGGGAAGG GACTGGAGTG GATTGGGTAT		127
DP71	GGAGTTGGAT CCGGCAGCCC CCAGGGAAGG GACTGGAGTG GATTGGGTAT		150
Consensus	GGAGTTGGAT CCGGCAGCCC CCAGGGAAGG GACTGGAGTG GATTGGGTAT		150
		CDR2	
4.17.3H	ATCTATTACA GTGGGAGCAC CAACTACAAC CCCTCCCTCA AGAGTCGAGT		177
DP71	ATCTATTACA GTGGGAGCAC CAACTACAAC CCCTCCCTCA AGAGTCGAGT		200
Consensus	ATCTATTACA GTGGGAGCAC CAACTACAAC CCCTCCCTCA AGAGTCGAGT		200
4.17.3H	CACCATATCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAGGT		227
DP71	CACCATATCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAGGT		250
Consensus	CACCATATCA GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAGGT		250
		CDR3	
4.17.3H	CTGTGACCGC TGC GGACACG GCCGTGTATT ACTGTGCCAG GACGTATAGC		277
DP71	CTGTGACCGC TGC GGACACG GCCGTGTATT ACTGTGCCAG GA-----		289
Consensus	CTGTGACCGC TGC GGACACG GCCGTGTATT ACTGTGCCAG GACGTATAGC		300
4.17.3H	AGTTCGTTCT ACTACTACGG TATGGACGTC TGGGGCCAAG GACACACGGT		327
DP71	-----	GA-----	293
Consensus	AGTTCGTTCT ACTACTACGG TATGGACGTC TGGGGCCAAG GACACACGGT		350
4.17.3H	CACCGTCTCC TCAG		341
DP71	-----		293
Consensus	CACCGTCTCC TCAG		364

FIG. 2D

Clone	C domain mutations	FR mutation	CDR mutation	Change in Cys	Change in glycosylation
2.13.2 Heavy	0	3	8	0	0
2.13.2 Light	0	1	4	1 (CDR3)	0
2.12.2 Heavy	0	2	8	0	0
2.12.2 Light	0	3	5	0	0

FIG. 3A

PF2 2.13.2 Heavy chain (DP-47(3-23)/D6-19/JH6)

MEFGLSHLPL VAILKGVQCE VQLLESGGGL VQPGSLRLS CTASGFTFSS YAMNVRQAP GKGLEHVSAL SSGGTFYA DSVKGRFTIS RDNSRTTLXL
 MEFGLSHLPL VAILKGVQCE VQLLESGGGL VQPGSLRLS CAASGFTFSS YAMNVRQAP GKGLEHVSAL SSGGSTYYA DSVKGRFTIS RDNSKNTLXL
 QKNSLRADT AVYICAK--D LGWSDSYYY YGMDVWGQGT TVTVSSASTK GPSVFPLAPC SRSTSESTAA LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP
 QKNSLRADT AVYICAKGYS SCW--YYY YGMDVWGQGT TVTVSSASTK GPSVFPLAPC SRSTSESTAA LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP
 VLQSSGLYS LSSVTVVPSS NFGTQTYTCN VDHKPSNTKV DKTVERKCCV ECPPCPAPPV AGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVQF
 VLQSSGLYS LSSVTVVPSS NFGTQTYTCN VDHKPSNTKV DKTVERKCCV ECPPCPAPPV AGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVQF
 NHYVDGVEVH NAKTKPREEQ FNSTFRVSV LTVVHQDHLN GKEYKCKVSN KGLPAPIEKT ISKTKGQPRE PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS
 NHYVDGVEVH NAKTKPREEQ FNSTFRVSV LTVVHQDHLN GKEYKCKVSN KGLPAPIEKT ISKTKGQPRE PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS
 DIAVEHESNG QPENNYKTP PMLDSGSGFF LYSKLTVDKS RHOQGNVFSC SVMHEALHNN YTKSLSLSP GK
 DIAVEHESNG QPENNYKTP PMLDSGSGFF LYSKLTVDKS RHOQGNVFSC SVMHEALHNN YTKSLSLSP GK

FIG. 3B

PF2 2.13.2 LC (A30/JK2) * . .

MDNRVPAOLL GLLLLHPPGA RCDIQNTQPP SLSASVGD R VTITCRASQG IRNDLCHYQQ KPGKAPKRLI YAA SRLHRGV PSRPSGSGSG TEPTLTISSL
MDNRVPAOLL GLLLLHPPGA RCDIQNTQSP SLSASVGD R VTITCRASQG IRNDLCHYQQ KPGKAPKRLI YAA SSLQSGV PSRPSGSGSG TEPTLTISSL
* . .

QPEDFATYYC LQNSYPCSF GQGTKLEIKR TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQH KVDNALQSGN SQESVTEQDS KDSTYSLSST
QPEDFATYYC LQNSYPYTF GQGTKLEIKR TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQH KVDNALQSGN SQESVTEQDS KDSTYSLSST

PLSKADY EK HKVYACEVTH QGLSSPVTKS FNRGEC
LTLSKADY EK HKVYACEVTH QGLSSPVTKS FNRGEC

FIG. 3C

PF2 2.12.1 Heavy chain (DP-35 (3-11)/D3-3/JH6) * . .

MEFGLSWVFL VAIKGVQCQ AQLVESGGGL VKPGSLRLS CAASGTFSD YMSWIRQAP GKGLEHVS YI SSSGSTRDYA DSVKGRFTIS RDNAKNSLYL
MEFGLSWVFL VAIKGVQCQ VQLVESGGGL VKPGSLRLS CAASGTFSD YMSWIRQAP GKGLEHVS YI SSSGSTIYYA DSVKGRFTIS RDNAKNSLYL
*

QKNSLRADT AVYICVR--D GVETTF-YYY YIGMDVHCQQ TTVTVSSAST KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSHNS GALTSGVHTF
QKNSLRADT AVYICARVLR FLEMLLYYY YIGMDVHCQQ TTVTVSSAST KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSHNS GALTSGVHTF

PAVLQSSGLY SLSSVTVTPS SNFGTQTYTC NVDHKPSNTK VDKTVERKCC VECPPCPAPP VAGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVQ
PAVLQSSGLY SLSSVTVTPS SNFGTQTYTC NVDHKPSNTK VDKTVERKCC VECPPCPAPP VAGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVQ

NWYVDGVEV HNAKTPREE QFNSTFRVVS VLTVVHQDHL NGKEYCKVS NKGLPAPIEK TISKTGQPRE PQVYTLPPS REEMTKNQVS LTCLVKGFYP
FNWYVDGVEV HNAKTPREE QFNSTFRVVS VLTVVHQDHL NGKEYCKVS NKGLPAPIEK TISKTGQPRE PQVYTLPPS REEMTKNQVS LTCLVKGFYP

SDIAVEHESN GPENNYKTT PPM LDSGSP FLYSKLTVDK SRHQQGNVFS CSVMHEALHN HYTKSLSLSP GK
SDIAVEHESN GPENNYKTT PPM LDSGSP FLYSKLTVDK SRHQQGNVFS CSVMHEALHN HYTKSLSLSP GK

FIG. 3D

PF2.12.1 Light chain (A30/Jx1)

MDMRVPAQLL	GLLLHFP	GA	RCDIQMTQSP	SSLSASVGDR	VTFTCRASQD	IRNDLGWYQQ	KPGKAPKRLI	YAA SRLQSGV	PSRPSGSGSG	TEPTLTIS
MDMRVPAQLL	GLLLHFP	GA	RCDIQMTQSP	SSLSASVGDR	VTITCRASQD	IRNDLGWYQQ	KPGKAPKRLI	YAA S SLQSGV	PSRPSGSGSG	TEPTLTIS
QPEDPATYYC	LQDN	YPTT	GQGTVEVIR	TVAAPSVFIF	PPSDEQLKSG	TASVVCLLN	FYPREAKVQH	KVDNALQSGN	SQESVTEQDS	KDSTYSLSST
QPEDPATYYC	LQDN	SYPTT	GQGTVEVIR	TVAAPSVFIF	PPSDEQLKSG	TASVVCLLN	FYPREAKVQH	KVDNALQSGN	SQESVTEQDS	KDSTYSLSST
LTLSKADYK	HKVYACEVTH	QGLSSPVTKS	FNRGEC							
LTLSKADYK	HKVYACEVTH	QGLSSPVTKS	FNRGEC							

FIG. 3E

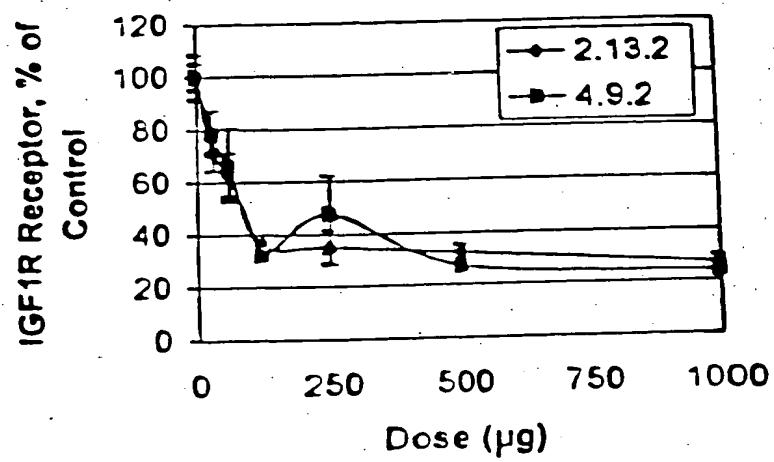


FIG. 4

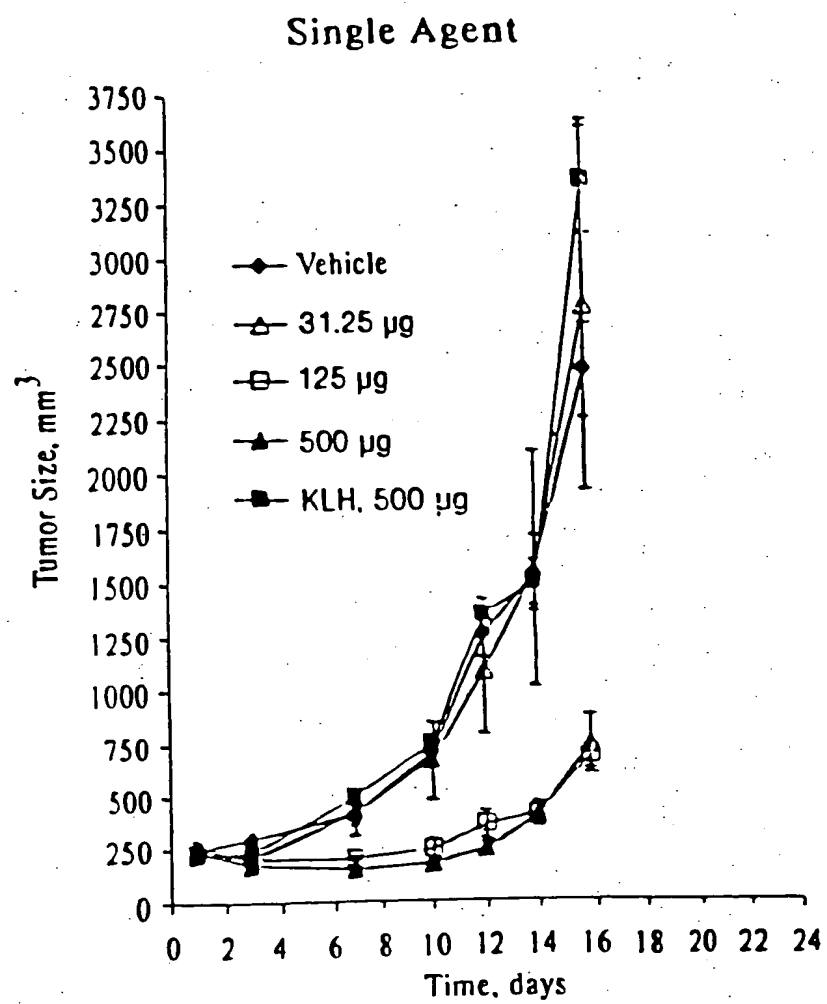


FIG. 5